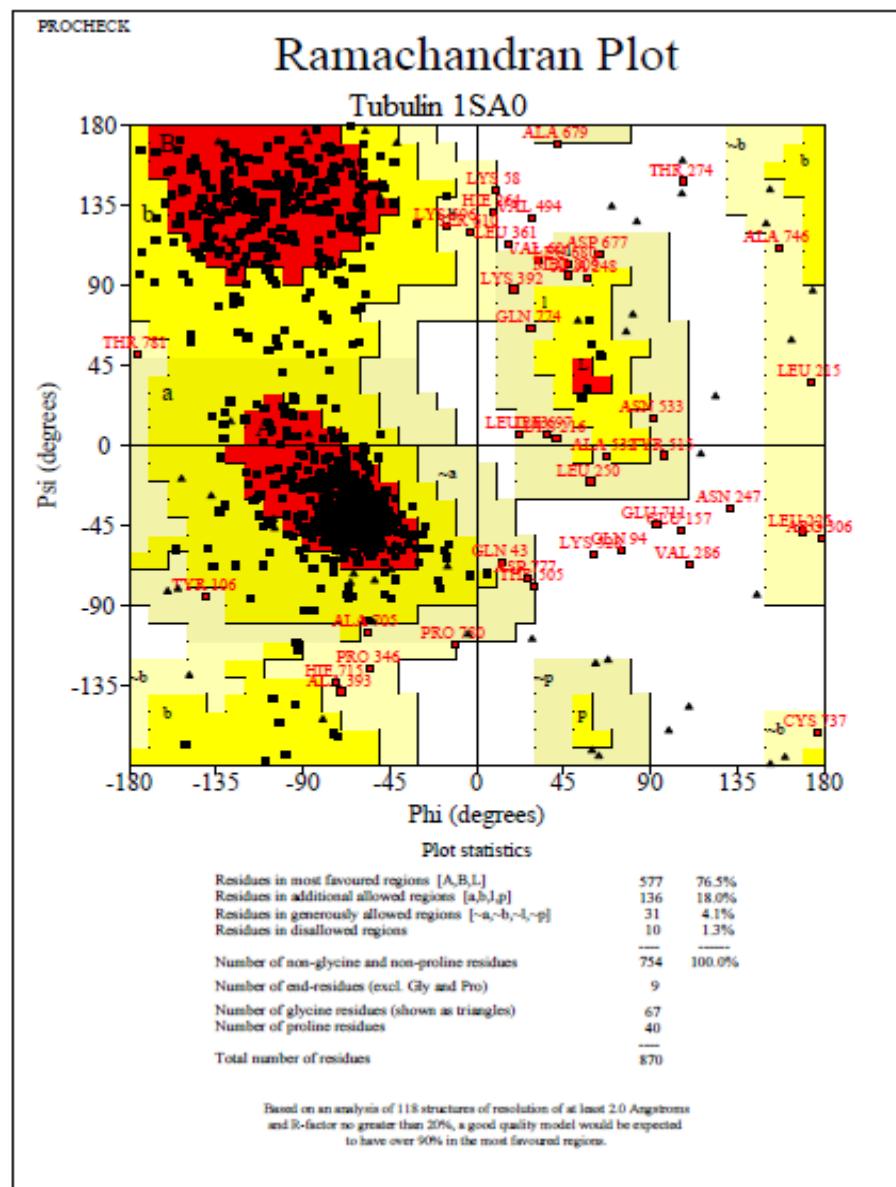
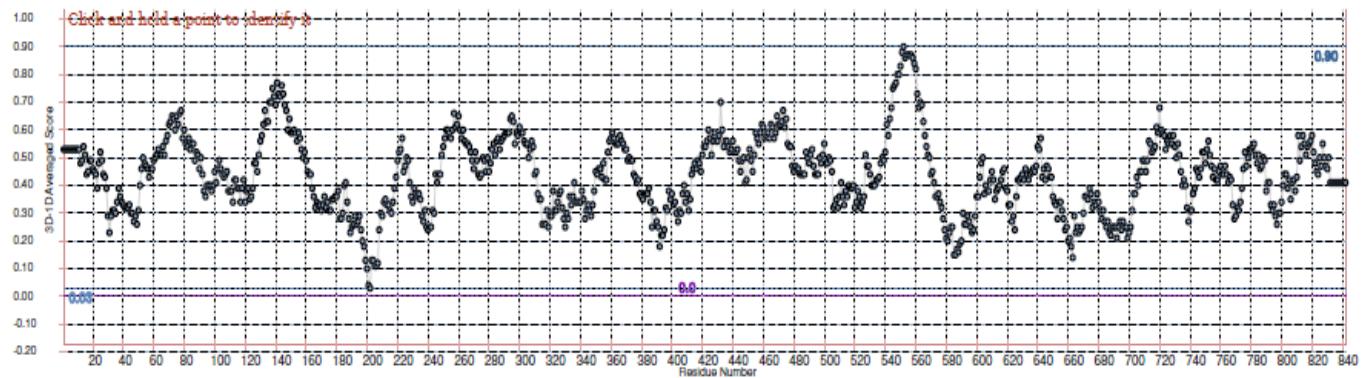


S1 Fig.



(A)

Verify 3D graph of Tubulin 1SA0



(B)

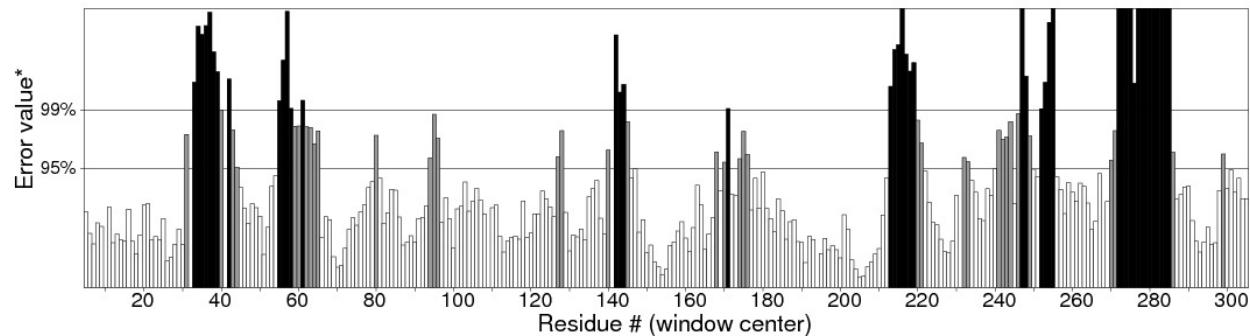
Program: ERRAT2

Errat score of Tubulin 1SA0

File: /var/www/SAVES/Jobs/5337210//errat.pdb

Chain#:1

Overall quality factor**: 77.251



*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.

**Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3A) the average overall quality factor is around 91%.

(C)